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Report Title

Final Report: Understanding Microbial Communities: Function, Structure and Dynamics

ABSTRACT

This grant partially supported a 4-month scientific programme 'Understanding microbial communities: Function, structure and dynamics', at the Isaac Newton Institute, University of Cambridge, United Kingdom, from August to December 2014. The programme involved over 150 participants, 3 workshops, 1 PhD school and 1 business day.

Enter List of papers submitted or published that acknowledge ARO support from the start of the project to the date of this printing. List the papers, including journal references, in the following categories:

(a) Papers published in peer-reviewed journals (N/A for none)

Received	<u>Paper</u>			
TOTAL:				
Number of Paper	s published in peer-reviewed journals:			
	(b) Papers published in non-peer-reviewed journals (N/A for none)			
Received	<u>Paper</u>			
TOTAL:				
Number of Papers published in non peer-reviewed journals:				

(c) Presentations

Number of Presentations: 0.00				
	Non Peer-Reviewed Conference Proceeding publications (other than abstracts):			
Received	<u>Paper</u>			
TOTAL:				
Number of Non	Peer-Reviewed Conference Proceeding publications (other than abstracts):			
	Peer-Reviewed Conference Proceeding publications (other than abstracts):			
Received	<u>Paper</u>			

Number of Peer-Reviewed Conference Proceeding publications (other than abstracts):

(d) Manuscripts

Received Paper

TOTAL:

1.00 Stefanie Widder, Rosalind Allen, Thomas Pfeiffer, Thomas P. Curtis, Carsten Wiuf, William T. Sloan, Otto X. Cordero, Sam P. Brown, Babak Momeni, Wenying Shou, Helen Kettle, Harry J. Flint, Andreas F. Haas, Béatrice Laroche, Jan-Ulrich Kreft, Paul B. Rainey, Shiri Freilich, Stefan Schuster, Kim Milferstedt, Jan R. van der Meer, Tobias Grosskopf, Jef Huisman, Andrew Free, Cristian Picioreanu, Christopher Quince, Isaac Klapper, Simon Labarthe, Barth F. Smets, Harris Wang, Orkun S. Soyer, Steven D. Allison, James Chong, Marco Cosentino-Lagomarsino, Ottavio A. Croze, Jérôme Hamelin, Jérôme Harmand, Rebecca Hoyle, Terence T. Hwa, Qusheng Jin, David R. Johnson, Víctor de Lorenzo, Mauro Mobilia, Barry Murphy, François Peaudecerf, James I. Prosser, Robert A. Quinn, Markus Ralser, Alison G. Smith, Jean-Philippe Steyer, Neil Swainston, Corina E. Tarnita, Eric Trably, Patrick B. Warren, Paul Wilmes. Challenges in Microbial Ecology: building predictive understanding, ISME Journal (06 2015)

TOTAL: 1

Number of Ma	nnuscripts:		
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Received	<u>Book</u>		
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Received	Book Chapter		
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		Patents Submitted	
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Names of Faculty Supported NAME PERCENT SUPPORTED **FTE Equivalent: Total Number:** Names of Under Graduate students supported NAME PERCENT SUPPORTED **FTE Equivalent: Total Number: Student Metrics** This section only applies to graduating undergraduates supported by this agreement in this reporting period The number of undergraduates funded by this agreement who graduated during this period: 0.00 The number of undergraduates funded by this agreement who graduated during this period with a degree in science, mathematics, engineering, or technology fields:..... 0.00 The number of undergraduates funded by your agreement who graduated during this period and will continue to pursue a graduate or Ph.D. degree in science, mathematics, engineering, or technology fields:..... 0.00 Number of graduating undergraduates who achieved a 3.5 GPA to 4.0 (4.0 max scale):..... 0.00 Number of graduating undergraduates funded by a DoD funded Center of Excellence grant for Education, Research and Engineering:..... 0.00 The number of undergraduates funded by your agreement who graduated during this period and intend to work for the Department of Defense 0.00 The number of undergraduates funded by your agreement who graduated during this period and will receive scholarships or fellowships for further studies in science, mathematics, engineering or technology fields: 0.00 Names of Personnel receiving masters degrees NAME **Total Number:** Names of personnel receiving PHDs **NAME Total Number:** Names of other research staff PERCENT SUPPORTED NAME **FTE Equivalent:**

Total Number:

Inventions (DD882)

Scientific Progress

See Attachment

Technology Transfer

As part of the programme we held a one day 'Open for business' day which was attended by both industrial representatives interested in microbial ecology and academics.

Final progress report

Foreword

This grant provided partial support for a 4-month scientific programme 'Understanding Microbial Communities: Function, Structure and Dynamics', at the Isaac Newton Institute, Cambridge University, UK, from 19th August 2014 – 19th December 2014. The organizers of the programme were Orkun Soyer (University of Warwick, UK), Rosalind Allen (University of Edinburgh, UK, PI on this grant), Tom Curtis (University of Newcastle, UK), Thomas Pfeiffer (Massey University, New Zealand), Bill Sloan (University of Glasgow, UK) and Carsten Wiuf (University of Copenhagen, Denmark). Here we report the key achievements of this programme.

Statement of problem

Microbes – single-celled, microscopic living organisms - make up the most of the biomass on earth and are found in all types of habitats, including soils, oceans, and surfaces and inside the bodies of higher organisms such as plants and humans. It is almost never the case that such habitats are occupied by a single microbial species, but rather they are home to many species of microbes that co-exist as a *microbial community*. Recent technological developments in DNA sequencing allow us to characterise the species composition of these communities from a variety of environmentally and medically-relevant habitats. Despite this explosive accumulation of data, there is an enormous gap between the levels of our empirical knowledge of microbial communities' composition and our experimental and theoretical understanding of their function, structure, and dynamics. Key unresolved questions are; do microbial communities achieve a higher-level function? how is this function stabilised? what are driving evolutionary and ecological processes of community function? what determines the level of complexity in microbial communities? Could simpler and minimal communities for a given function be developed and stably maintained?

Recent technological advances have greatly improved our ability to determine which microbes are present in a given sample via DNA sequencing. However, it will not be possible to answer many of these questions with only such empirical data on microbial community species composition. To really understand microbial communities, we will need additional data on functional traits within communities and their temporal and spatial distribution. More importantly, however, we also need theoretical frameworks that will provide the necessary grounding for evaluating the biological data and develop testable hypotheses. The development of these theoretical frameworks will hinge on the interactions between mathematics, physics and microbial ecology.

The primary purpose of this program was to facilitate the building a scientific community around using and developing mathematical approaches for understanding microbial communities. This is a timely undertaking, as accumulation of data on microbial communities has been continuing for about a decade and the field is starting to attract attention from both experimental and theoretical groups. In addition, a diverse array of funding bodies, as well as industry partners, have started to appreciate the importance and potential of microbial communities for increased understanding of biology and advancement of new biotechnologies and medical applications.

Summary of results

(a) Activities

Over the course of the 4 months of the program (from August to December), the Isaac Newton Institute hosted over 150 scientists with a diverse set of backgrounds in mathematics, physics, microbiology, ecology, economics, and computer science. To facilitate the interaction of these scientists, we held bi-weekly informal seminars and daily social events, in addition to three scientific workshops, one PhD school and one industry-academia day.

The scientific workshops hosted by our program were

Workshop 1: "Interdisciplinary approaches to understanding microbial communities", 10-12 September 2014. This workshop focused on identifying the key challenges in modeling and experimental analysis of microbial communities.

Workshop 2: "Structure, function and dynamics in microbial communities", 30-31 October 2014. This workshop explored in more detail the experimental and mathematical tools that are needed to model microbial communities, focusing on evolution, ecology and dynamics.

Workshop 3: "Engineering and control of natural and synthetic microbial communities"

This workshop explored how we can usefully engineer synthetic communities from scratch and manipulate existing communities, for bioremediation and other biotechnological applications.

Our PhD summer school "Methods for mathematical and empirical analysis of microbial communities", took place on 27-29 October 2014, and featured tutorial-style lectures from leading scientists in the field and allowing PhD students to make connections which will be important in their later careers. There were also ~10 short talks by early-career scientists as well as a poster session. Several of these early career scientists spent extended time at the Institute, developing their own ideas and interacting with the more established scientists who were participating in the programme.

The importance of microbial communities for health, industry and the natural environment cannot be overstated. This potential was explored with an "Open Business Event" in December 2014, where industrialists, academics and regulators came together to evaluate the industrial and medical potential of the emerging field of microbial communities research.

(b) Scientific outcomes.

The key scientific outcome of the programme was the establishment of contacts among disparate scientist coming from different fields. It is quite possible that the programme will be seen as a crucial point in the development and expansion of the field of modelling in microbial ecology and in particular the modelling of microbial communities. In line with this expectation, almost all of the participants were enthusiastic about participating in the development of a jointly authored review paper that could help shape the future of the field. This paper [1] is now in the submission stage and lists over 50 co-authors.

Overall, it can be confidently stated that the program has brought the majority of scientists currently working on or interested in microbial communities together. Among the 41% of the respondents to the post-programme questionnaire, 90% of them rated the programme excellence at above 80%. Specific comments of these participants highlighted the success of the event,

particularly, in terms of networking and connecting empirical and theoretical scientists. The majority of respondents stated that they have become aware of new research questions and contacts as a result of the programme.

In addition to the many individual interactions between scientists that took place during its 4-month duration, the programme has also had an impact on the wider scientific community. This is perhaps most evident in the fact that the UK Biosciences and Biotechnology Research Council recently announced the focus area of their current strategic funding with the same title as the program; "Understanding Microbial Communities". We have confirmed that this decision was partly inspired by the activity of this program.

The program website remains available via the Isaac Newton Institute's website at www.newton.ac.uk. As well as listing all workshop speakers and other programme participants, this website also provides access to recordings of all seminars and workshop talks which took place during the programme.

Bibliography

[1] Widder, S., Allen R., et al. (2015) 'Challenges in microbial ecology: building predictive understanding of community function and dynamics', review article submitted to *ISME Journal*.